1600

RAW SEQUENCE LISTING DATE: 01/08/2003
PATENT APPLICATION: **US/09/645,078** TIME: 10:59:44

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

```
      4 <110> APPLICANT: Bistrup, Annette
      5       Rosen, Steven
      6       Tangemann, Kirsten
      7       Hemmerich, Stefan
     10 <120> TITLE OF INVENTION: HEC-G1cNAc6ST
     13 <130> FILE REFERENCE: UCAL-107CIP2
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/645,078
C--> 16 <141> CURRENT FILING DATE: 2002-12-19
     18 <150> PRIOR APPLICATION NUMBER: PCT/US99/04316
     19 <151> PRIOR FILING DATE: 1998-02-26
     21 <150> PRIOR APPLICATION NUMBER: US 09/190,911
     22 <151> PRIOR FILING DATE: 1998-11-12
     24 <150> PRIOR APPLICATION NUMBER: US 09/045,284
     25 <151> PRIOR FILING DATE: 1998-03-20
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     29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     31 <210> SEQ ID NO: 1
     32 <211> LENGTH: 2043
     33 <212> TYPE: DNA
     34 <213> ORGANISM: HOMO SAPIENS
     36 <400> SEQUENCE: 1
     37 gaattccatt gtgttgggta cggaagacga cagaagggta gaggagaaaa gcgcatggcc 60
     38 cggctagcag tgagcctctc aaaagcagca gggaagccca agccacaagg tcttccactt 120
     39 cagcacaatg ctactgccta aaaaaatgaa gctcctgctg tttctggttt cccagatggc 180
     40 catcttggct ctattcttcc acatgtacag ccacaacatc agctccctgt ctatgaaggc 240
     41 acagcccgag cgcatgcacg tgctggttct gtcttcctgg cgctctggct cttcttttgt 300
     42 ggggcagctt tttgggcagc acccagatgt tttctacctg atggagcccg cctggcacgt 360
     43 gtggatgacc ttcaagcaga gcaccgcctg gatgctgcac atggctgtgc gggatctgat 420
     44 acgggccgtc ttcttgtgcg acatgagcgt ctttgatgcc tacatggaac ctggtccccg 480
     45 gagacagtcc agcctctttc agtgggagaa cagccgggcc ctgtgttctg cacctgcctg 540
     46 tgacatcatc ccacaagatg aaatcatccc ccgggctcac tgcaggctcc tgtgcagtca 600
     47 acagcccttt gaggtggtgg agaaggcctg ccgctcctac agccacgtgg tgctcaagga 660
     48 ggtgcgcttc ttcaacctgc agtccctcta cccgctgctg aaagacccct ccctcaacct 720
     49 gcatatcgtg cacctggtcc gggacccccg ggccgtgttc cgttcccgag aacgcacaaa 780
     50 gggagatctc atgattgaca gtcgcattgt gatggggcag catgagcaaa aactcaagaa 840
     51 ggaggaccaa ccctactatg tgatgcaggt catctgccaa agccagctgg agatctacaa 900
     52 gaccatccag tccttgccca aggccctgca ggaacgctac ctgcttgtgc gctatgagga 960
     53 cctggctcga gcccctgtgg cccagacttc ccgaatgtat gaattcgtgg gattggaatt 1020
     54 cttgccccat cttcagacct gggtgcataa catcacccga ggcaagggca tgggtgacca 1080
     55 cgctttccac acaaatgcca gggatgccct taatgtctcc caggcttggc gctggtcttt 1140
     56 gccctatgaa aaggtttctc gacttcagaa agcctgtggc gatgccatga atttgctggg 1200
     57 ctaccgccac gtcagatctg aacaagaaca gagaaacctg ttgctggatc ttctgtctac 1260
     58 ctggactgtc cctgagcaaa tccactaaga gggttgagaa ggctttgctg ccacctggtg 1320
```

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59 tcagcctcag tcactttctc tgaatgcttc tgagccttgc ctacatctct gagccttaac 1380
60 tacatgtctg tgggtatcac actgagtgtg agttgtgtcc acacgtgctc aagcagaagg 1440
61 acttttgtgt ccatgcttgt gtctagaaaa cagactgggg aaccttatgt gagcagcaca 1500
62 tcccaccagt gaaacagggt attgctcttc ttcttttctt gatcttcctg tctgggcaga 1560
63 cttcagagac tttgtggcct ggaggcctat taagcacgac acagtatcag tggaattgat 1620
64 ccataaacct ccctgtccac atcttgccca atggggaatg gatctttcac caaagagctc 1680
65 accagcattt tccacagaga tgcgaattct gagcccttgg agttcccaat gggattcaag 1740
66 gaaggaagtg ggaacaaggt tggatgccta cttatgagct tgaccataca gctatcggta 1800
67 atcagaaata tgaaacaaaa tctctgacaa aagagcaagc tcttaagttc acaaggtgcc 1860
68 tgggcttgat ttgaatatca tttccctttg cattttccca ttacatagaa aactttgacc 1920
69 tgtgaaactt gccatctgtt aatactaaaa ttcccaaata aggttctgtt tagaatgtcc 1980
70 ctttttatgc ttcttaatta ttagcagtaa atgttcattt ttatgggatc ctaaaaaaaa 2040
71 aaa 2043
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 386
75 <212> TYPE: PRT
76 <213> ORGANISM: HOMO SAPIENS
78 <400> SEQUENCE: 2
79 Met Leu Leu Pro Lys Lys Met Lys Leu Leu Leu Phe Leu Val Ser Gln
80 1 5 10 15
81 Met Ala Ile Leu Ala Leu Phe Phe His Met Tyr Ser His Asn Ile Ser
82 20 25 30
83 Ser Leu Ser Met Lys Ala Gln Pro Glu Arg Met His Val Leu Val Leu
84 35 40 45
85 Ser Ser Trp Arg Ser Gly Ser Ser Phe Val Gly Gln Leu Phe Gly Gln
86 50 55 60
87 His Pro Asp Val Phe Tyr Leu Met Glu Pro Ala Trp His Val Trp Met
88 65 70 75 80
89 Thr Phe Lys Gln Ser Thr Ala Trp Met Leu His Met Ala Val Arg Asp
90 85 90 95
91 Leu Ile Arg Ala Val Phe Leu Cys Asp Met Ser Val Phe Asp Ala Tyr
92 100 105 110
93 Met Glu Pro Gly Pro Arg Arg Gln Ser Ser Leu Phe Gln Trp Glu Asn
94 115 120 125
95 Ser Arg Ala Leu Cys Ser Ala Pro Ala Cys Asp Ile Ile Pro Gln Asp
96 130 135 140
97 Glu Ile Ile Pro Arg Ala His Cys Arg Leu Leu Cys Ser Gln Gln Pro
98 145 150 155 160
99 Phe Glu Val Val Glu Lys Ala Cys Arg Ser Tyr Ser His Val Val Leu
100 165 170 175
101 Lys Glu Val Arg Phe Phe Asn Leu Gln Ser Leu Tyr Pro Leu Leu Lys
102 180 185 190
103 Asp Pro Ser Leu Asn Leu His Ile Val His Leu Val Arg Asp Pro Arg
104 195 200 205
105 Ala Val Phe Arg Ser Arg Glu Arg Thr Lys Gly Asp Leu Met Ile Asp
106 210 215 220
107 Ser Arg Ile Val Met Gly Gln His Glu Gln Lys Leu Lys Lys Glu Asp
108 225 230 235 240
109 Gln Pro Tyr Tyr Val Met Gln Val Ile Cys Gln Ser Gln Leu Glu Ile

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Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

```
110                 245                 250                 255
111 Tyr Lys Thr Ile Gln Ser Leu Pro Lys Ala Leu Gln Glu Arg Tyr Leu
112             260                 265                 270
113 Leu Val Arg Tyr Glu Asp Leu Ala Arg Ala Pro Val Ala Gln Thr Ser
114         275                 280                 285
115 Arg Met Tyr Glu Phe Val Gly Leu Glu Phe Leu Pro His Leu Gln Thr
116     290                 295                 300
117 Trp Val His Asn Ile Thr Arg Gly Lys Gly Met Gly Asp His Ala Phe
118 305                 310                 315                 320
119 His Thr Asn Ala Arg Asp Ala Leu Asn Val Ser Gln Ala Trp Arg Trp
120                 325                 330                 335
121 Ser Leu Pro Tyr Glu Lys Val Ser Arg Leu Gln Lys Ala Cys Gly Asp
122             340                 345                 350
123 Ala Met Asn Leu Leu Gly Tyr Arg His Val Arg Ser Glu Gln Glu Gln
124         355                 360                 365
125 Arg Asn Leu Leu Leu Asp Leu Leu Ser Thr Trp Thr Val Pro Glu Gln
126     370                 375                 380
127 Ile His
128 385
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 1926
133 <212> TYPE: DNA
134 <213> ORGANISM: MOUSE
136 <400> SEQUENCE: 3
137 gggcatctaa cttacacttg gtcagacaag acaagctttt gcctacaaag gccacactct 60
138 gtcaggggtg tagaaaggtg tggggtgtgg cagaactccc tatagtgatt aaatgtgctg 120
139 ggtaggatat tctcggtggt ttgatggatg agaaagccca gagggtgagt tttaaagact 180
140 tgtaacatag aatgcagtga tccaattaag agccagaatt actttgcaga gggatctgga 240
141 caaatacttg caggaatgtt tttggttttt gtttgtttgt ttgtttgttt tacattgctc 300
142 cttggatggg aatccagaga agcccgaagg tagatgctgt aacaacctaa ctcagcccca 360
143 tcccctctgc ttgctctttc aaggtcttct ccttcttccg caggatgatg ctgttgaaga 420
144 aagggaggct gctgatgttc ctgggttccc aggtcatcgt tgtagctctc ttcatccata 480
145 tgtccgtcca cagacacctt tcccagaggg aggagtccag gaggcccgtg catgtgctgg 540
146 tgctgtcttc ctggcggtca ggatcctctt ttgtgggaca gcttttcggg cagcacccgg 600
147 atgtgttcta cctgatggag cctgcctggc atgtgtggat gactttcacc agcagcacag 660
148 cctggaagct gcacatggct gtgcgggatc ttctgcgttc cgtcttcctg tgtgacatga 720
149 gcgtctttga tgcctacatg aacccaggcc cccggaaaca gtccagcctc ttccagtggg 780
150 agcaaagccg ggccctgtgc tcagcgcctg tgtgtgactt cttccctgcc cacgagatca 840
151 gctcacccaa gcactgcaag ctgctctgcg gtcagcagcc ctttgatatg gtggagaagg 900
152 cctgccgctc tcacggcttc gtggtactca aggaggtgcg ttttctcagc ctgcaggccc 960
153 tctatccact actcacggac ccttccctca acctgcacgt cgtgcacctg gtccgagacc 1020
154 cccgggccgt gttccgatcc cgggagcaca ccaccataga actcatggtt gacagtcata 1080
155 ttgtgctagg gcagcatttg gaaacgatca aggaggaaga ccagccctat tatgccatga 1140
156 agatcatctg caaaagccag gtggacatag tcaaggccat ccaaaccctc cctgaagctc 1200
157 tgcagcagcg ctacctgttc ctgaggtatg aggacctggt tcgggcaccc ctggcccaga 1260
158 cgaccagact atataaattt gtggggttgg atttttgcc ccacctccaa acatgggttt 1320
159 acaatgtcac ccgcggcaag ggcatgggtc agcatgcctt ccatactaac gccaggaacg 1380
160 ccctcaacgt ctctcaggcg tggcgttggt ccttacctta cgaaaaggtt tcccagcttc 1440
161 aagatgcctg cggtgaggct atggatttgc tgggatacct ccaggtcaga tctcaacaag 1500
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RAW SEQUENCE LISTING DATE: 01/08/2003
PATENT APPLICATION: **US/09/645,078** TIME: 10:59:44

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

```
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gagaaggtta aggaggtctg tctgcacccc ttggttccag ccttagtcac cattaaacgc 1620
acagaagcct taaggtataa ccaaactgag tgccccttc tcctcagccc caagcagagg 1680
ggtctttgtg tctatactca tgtctaccct acaactgagc ctaaaaagcc aagaaacagt 1740
atctttctgt cttgaaaata cttaggaacc ttaagcagcc cctttgacct gtcaagcaag 1800
actttcttgt aaccttggcc ttcttacctg tgcatacctt ggagactcgg tctggaggca 1860
tactggacac agcaaacagc atctgtggag tgtgtctgta aacctccctg tcacatcttt 1920
tctaag                                                           1926

<210> SEQ ID NO: 4
<211> LENGTH: 388
<212> TYPE: PRT
<213> ORGANISM: MOUSE
<400> SEQUENCE: 4
Met Met Leu Leu Lys Lys Gly Arg Leu Leu Met Phe Leu Gly Ser Gln
 1               5                  10                  15
Val Ile Val Val Ala Leu Phe Ile His Met Ser Val His Arg His Leu
            20                  25                  30
Ser Gln Arg Glu Glu Ser Arg Arg Pro Val His Val Leu Val Leu Ser
        35                  40                  45
Ser Trp Arg Ser Gly Ser Ser Phe Val Gly Gln Leu Phe Gly Gln His
    50                  55                  60
Pro Asp Val Phe Tyr Leu Met Glu Pro Ala Trp His Val Trp Met Thr
65                  70                  75                  80
Phe Thr Ser Ser Thr Ala Trp Lys Leu His Met Ala Val Arg Asp Leu
                85                  90                  95
Leu Arg Ser Val Phe Leu Cys Asp Met Ser Val Phe Asp Ala Tyr Met
            100                 105                 110
Asn Pro Gly Pro Arg Lys Gln Ser Ser Leu Phe Gln Trp Glu Gln Ser
        115                 120                 125
Arg Ala Leu Cys Ser Ala Pro Val Cys Asp Phe Phe Pro Ala His Glu
    130                 135                 140
Ile Ser Ser Pro Lys His Cys Lys Leu Leu Cys Gly Gln Gln Pro Phe
145                 150                 155                 160
Asp Met Val Glu Lys Ala Cys Arg Ser His Gly Phe Val Val Leu Lys
                165                 170                 175
Glu Val Arg Phe Leu Ser Leu Gln Ala Leu Tyr Pro Leu Leu Thr Asp
            180                 185                 190
Pro Ser Leu Asn Leu His Val Val His Leu Val Arg Asp Pro Arg Ala
        195                 200                 205
Val Phe Arg Ser Arg Glu His Thr Thr Ile Glu Leu Met Val Asp Ser
    210                 215                 220
His Ile Val Leu Gly Gln His Leu Glu Thr Ile Lys Glu Glu Asp Gln
225                 230                 235                 240
Pro Tyr Tyr Ala Met Lys Ile Ile Cys Lys Ser Gln Val Asp Ile Val
                245                 250                 255
Lys Ala Ile Gln Thr Leu Pro Glu Ala Leu Gln Gln Arg Tyr Leu Phe
            260                 265                 270
Leu Arg Tyr Glu Asp Leu Val Arg Ala Pro Leu Ala Gln Thr Thr Arg
        275                 280                 285
```

RAW SEQUENCE LISTING DATE: 01/08/2003
PATENT APPLICATION: **US/09/645,078** TIME: 10:59:44

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

```
213 Leu Tyr Lys Phe Val Gly Leu Asp Phe Leu Pro His Leu Gln Thr Trp
214     290                 295                 300
215 Val Tyr Asn Val Thr Arg Gly Lys Gly Met Gly Gln His Ala Phe His
216 305                 310                 315                 320
217 Thr Asn Ala Arg Asn Ala Leu Asn Val Ser Gln Ala Trp Arg Trp Ser
218                 325                 330                 335
219 Leu Pro Tyr Glu Lys Val Ser Gln Leu Gln Asp Ala Cys Gly Glu Ala
220             340                 345                 350
221 Met Asp Leu Leu Gly Tyr Leu Gln Val Arg Ser Gln Gln Glu Gln Gly
222         355                 360                 365
223 Asn Leu Ser Leu Asp Leu Leu Ser Ser Ser His Ile Leu Gly Gln Val
224     370                 375                 380
225 Phe Arg Glu Gly
226 385
229 <210> SEQ ID NO: 5
230 <211> LENGTH: 37
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: synthetic primer
237 <400> SEQUENCE: 5
238 aaactcaaga aggaggacca accctactat gtgatgc                          37
240 <210> SEQ ID NO: 6
241 <211> LENGTH: 47
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: synthetic primer
248 <400> SEQUENCE: 6
249 ataaagcttg tggatttgtt cagggacatt ccaggtagac agaagat               47
251 <210> SEQ ID NO: 7
252 <211> LENGTH: 29
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: synthetic primer
259 <400> SEQUENCE: 7
260 Thr Trp Tyr Thr Trp Tyr Cys Thr Ile Thr Trp Tyr Gly Ala Arg Cys
261  1               5                  10                  15
262 Cys Ile Cys Thr Ile Thr Gly Gly Cys Ala Tyr Ser Thr
263             20                  25
266 <210> SEQ ID NO: 8
267 <211> LENGTH: 59
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: synthetic primer
274 <400> SEQUENCE: 8
275 caagagtgtt ttctaaatac agtattgtag aaagtaattg ccaatagcat gagtctgga  59
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/08/2003
PATENT APPLICATION: **US/09/645,078** TIME: 10:59:45

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 1,2,9,11,14,16,17,18,21,23,26,27
Seq#:34; Xaa Pos. 2,4,5,6,7,14,15,16
Seq#:35; Xaa Pos. 2,3,5,6,7,9,10,17,18,19

VERIFICATION SUMMARY DATE: 01/08/2003
PATENT APPLICATION: **US/09/645,078** TIME: 10:59:45

Input Set : **D:\seqlist.txt**
Output Set: **N:\CRF4\01082003\I645078.raw**

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:579 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:583 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:587 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:591 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:595 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:599 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:603 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:607 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:611 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:615 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:619 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:16
L:640 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:644 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:648 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:652 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:656 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:660 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:664 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:683 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:687 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:691 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:695 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:703 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:707 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:711 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:715 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:16